

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 01:27:49 ; Search time 544.842 Seconds  
(without alignments)  
10849.659 Million cell updates/sec

Title: US-09-856-979-7  
Perfect score: 365  
Sequence: 1 tcagccagaccaatgggggc.....tccatcaagccgcgcgatg 365

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :				EST:*			
				1:	em_estba:*		
				2:	em_esthum:*		
				3:	em_estin:*		
				4:	em_estmu:*		
				5:	em_estov:*		
				6:	em_estpl:*		
				7:	em_estro:*		
				8:	em_hic:*		
				9:	gb_est1:*		
				10:	gb_est2:*		
				11:	gb_hic:*		
				12:	gb_est3:*		
				13:	gb_est4:*		
				14:	gb_est5:*		
				15:	em_estfun:*		
				16:	em_estom:*		
				17:	gb_gss:*		
				18:	em_gss_hum:*		
				19:	em_gss_inv:*		
				20:	em_gss_pln:*		
				21:	em_gss_vrt:*		
				22:	em_gss_fun:*		
				23:	em_gss_mam:*		
				24:	em_gss_mus:*		
				25:	em_gss_other:*		
				26:	em_gss_pro:*		
				27:	em_gss_rod:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	41	11.2	764	9	AL565922
2	39	10.7	391	14	C74001
3	37.8	10.4	571	10	BE044167
4	37.8	10.4	960	9	AL528127
5	37.8	10.4	966	9	AL528272
6	37.4	10.2	969	17	AZ551127
					ENTDN11TR

7	37.2	10.2	777	9	AL553672	AL553672
8	37	10.1	574	9	AU029306	AU029306
9	37	10.1	841	9	AL582386	AL582386
10	36.8	10.1	429	14	W44754	W44754
11	36.6	10.0	476	17	BH018696	BH018696
12	36.6	10.0	493	17	L2025Y	AL354102
13	36.6	10.0	916	9	AL564785	AL564785
14	36.4	10.0	1165	14	BM904449	BM904449
15	36.2	9.9	893	9	AL527787	AL527787
16	36.2	9.9	958	17	CNS044HE	AL274091
17	36.2	9.9	1028	9	AL545506	AL545506
18	35.8	9.8	957	9	AL574284	AL574284
19	35.8	9.8	995	9	AL562554	AL562554
20	35.6	9.8	994	13	BM459131	BM459131
21	35.6	9.8	1169	17	AG142795	AG142795
22	35.6	9.8	1327	12	BE914468	BE914468
23	35.4	9.7	519	17	BH233534	BH233534
24	35.4	9.7	912	9	AL563783	AL563783
25	35	9.6	430	12	BF733514	BF733514
26	35	9.6	452	12	BF733516	BF733516
27	35	9.6	484	14	BM697674	BM697674
28	35	9.6	561	13	BM507336	BM507336
29	35	9.6	570	13	BI717755	BI717755
30	35	9.6	585	14	BM830316	BM830316
31	35	9.6	586	14	BM769817	BM769817
32	35	9.6	639	10	BE263421	BE263421
33	35	9.6	644	10	AW391273	AW391273
34	35	9.6	657	14	BM769366	BM769366
35	35	9.6	670	14	BM726988	BM726988
36	35	9.6	671	13	BI222237	BI222237
37	35	9.6	706	14	BM718786	BM718786
38	35	9.6	716	14	BM769332	BM769332
39	35	9.6	787	12	BF348220	BF348220
40	35	9.6	794	12	EG402941	EG402941
41	35	9.6	802	12	BF862180	BF862180
42	35	9.6	832	13	BM006545	BM006545
43	35	9.6	863	13	BI766676	BI766676
44	35	9.6	864	12	BE893685	BE893685
45	35	9.6	883	14	BQ670113	BQ670113

ALIGNMENTS

RESULT 1	AL565922	AL565922	764 bp	mrna	linear	EST 16-FEB-2001
LOCUS	AL565922	LT1_FL013_FBrn1	Homo sapiens	cdna	clone	CS0DF009YG24 3
DEFINITION	prime, mRNA sequence.					
ACCESSION	AL565922					
VERSION	AL565922.1	GI:12917777				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage Bp 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.					
FEATURES	Location/Qualifiers					
source	1..764					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/clone="CS0DF009YG24"					
	/clone_lib="LT1_FL013_FBrn1"					
	/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"					
	/lab_host="DH10B"					

/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 199 a 184 c 227 g 130 t 24 others  
ORIGIN

Query Match 11.2%; Score 41; DB 9; Length 764;  
Best Local Similarity 50.3%; Pred. No. 0.21;  
Matches 74; Conservative 9; Mismatches 64; Indels 0; Gaps 0;

QY 172 GTGGACGCGTGAGGTGCTTTCGOCATGACCGTCCCTGGTTGTTGCAGTCACTTGGCGCAG 231

Db 597 GGGATYGAGACAGGTGGAGSTGAGGTGACTGSCCATGGCTSTATTCTGSACTTGTGGCAG 656

QY 232 CTTGCACCGTCACTCACCTGCCACATTGCCCGCGCTCGCGGCTACAAAAGCCAC 291

Db 657 CTGGACACAGGTCTGCTCTSCSTAATATATACSSAGSCASCYSACGCTCCAACCTGCCTC 716

QY 292 ACACGCACGCGGCCACGATACCCAT 318

Db 717 ATAGGACCGGACGACGCGGCCCTT 743

RESULT 2

C74001

LOCUS

DEFINITION C74001 Rice panicle shorter than 3cm Oryza sativa (japonica cultivar-group) cDNA clone E30132\_1A, mRNA sequence.

ACCESSION C74001

VERSION C74001.1 GI:2442230

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group).

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

TITLE Ehrhartoldeae; Oryzeae; Oryza.

JOURNAL 1 (bases 1 to 391)

COMMENT Sasaki,T. and Yamamoto,K.

Unpublished (1997)

Contact: Takuji Sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki

305-8602, Japan

Tel: 81-298-38-7441

Fax: 81-298-38-7468

Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/PROJECT="RGP".

PROJECT="RGP".

FEATURES

source

1..391

/organism="Oryza sativa (japonica cultivar-group)"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clone="E30132\_1A"

/clone\_lib="Rice panicle shorter than 3cm"

/dev\_stage="shorter than 3cm"

/note="Organ: panicle"

BASE COUNT 68 a 128 c 113 g 78 t 4 others

ORIGIN

Query Match 10.7%; Score 39; DB 14; Length 391;

Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 327 CCCGGTGCCAGCAAGAGATCCATCAAGCCGTCGGGATG 365

|||||

Db 1 CCCGGTGCCAGCAAGAGATCCATCAAGCCGTCGGGATG 39

RESULT 3

BE044167

LOCUS

DEFINITION

ho39e01.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:3039768 3' similar to SW:TISD\_HUMAN P47974 TIS11D PROTEIN ; , mRNA sequence.

ACCESSION BE044167

VERSION BE044167.1 GI:8361220

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 571)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Possible reversed clone: polyt not found

Seq primer: -400p from Gibco

High quality sequence stop: 514.

FEATURES

source

1..571

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3039768"

/clone\_lib="Soares\_NFL\_T\_GBC\_S1"

/lab\_host="DH10B"

/note="Organ: pooled; Vector: pT73b-Pac (Pharmacia) with

a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung NbHL19W, testis NHT, and B-cell

NCI-CGAP-GCBI) were mixed, and ss circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297480-302087, 682632-687239,

726408-728711, and 729096-731399. Subtraction by Bento

Soares and M. Fatima Bonaldo.

BASE COUNT 120 a 179 c 129 g 143 t

ORIGIN

Query Match 10.4%; Score 37.8; DB 10; Length 571;

Best Local Similarity 48.0%; Pred. No. 1.6;

Matches 108; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 136 CTTCTTTCACCGTGCTACTGTACATCCTGTAGACGGTGGACGGCTGAGGTGCTTTCGCC 195

|||||

Db 40 CTGCTGGCGCGGGGGCGCGCTGCGGGCGCTGCTGCGGCCCTCGTGGCCCAACACGCC 99

QY 196 ATGACCGTCTTGGTTGTTCAGTCACTTGGCGCAGCTTGCACCGTGAACCTGACCTACCTGCCAC 255

|||||

Db 100 TTCCGCTTCGGTCCGGAGCTCAGCAGCTCATCAGCCGCTCGCCATCCAGACCCACAC 159

QY 256 ATTGCCCGCGCGCTCGCGGGCGCTACAAAGCCACACACGCGCGCGCCGACGATACCC 315

|||||

Db 160 TTTGCCGCGCTGCGCGCGCGCGCTACTACCGAGCCAGCAGCAGTACCAACCACC 219

QY 316 CATCTAGCATCCCGGTGTCCAGCAAGAGATCCATCAAGCCGTCG 360

|||||

Db 220 ATTCCATCTCTTCACTTGAACAGCATTAGTTAAGTCCAGATGTGG 264

RESULT 4

```

AL528127
LOCUS       AL528127       960 bp      mRNA      linear      EST 13-FEB-2001
DEFINITION  AL528127 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC025YE12 3
prime, mRNA sequence.
ACCESSION   AL528127
VERSION     AL528127.1  GI:12791620
KEYWORDS    EST.
SOURCE      human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 960)
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES             Location/Qualifiers
     source           1..960
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DC025YE12"
                     /clone_lib="LTI_NFL003_NBC3"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed
                     by Life Technologies. Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"

BASE COUNT   250 a    241 c    285 g    178 t    6 others
ORIGIN

Query Match      10.4%;   Score 37.8;   DB 9;   Length 960;
Best Local Similarity 53.1%;   Pred. No. 2.2;
Matches 78;   Conservative 1;   Mismatches 68;   Indels 0;   Gaps 0;

QY  172  GTGGACCGGTGAGGTGCTTTTCGCCCATGACCGTCCTTGGTTGTTGCAGTCACCTTGGCGCAG 231
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   685  GGGATCGAGAGAGGTGGAGGTGAGGTGACTGGCCATGGCTGTATTCTGGACTTGTGGCAG 744
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY  232  CTTGCACCGTGACTCACCTGCCACATTGCCCGCCCGCTCGCGCGCGCCCTACAAAGCCAC 291
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   745  CTGGGACAGGGTCTGCTCTCGCTAATTATACCGGAGGCGAGCTGCAGCTGCAACTGCCTC 804
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY  292  ACAGGCACGCGCGGCCACGATAACCCAT 318
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   805  ATAGGACCGGGCAGCAGCAGCGCCTT 831
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
AL528272
LOCUS       AL528272       966 bp      mRNA      linear      EST 13-FEB-2001
DEFINITION  AL528272 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC023Y013 3
prime, mRNA sequence.
ACCESSION   AL528272
VERSION     AL528272.1  GI:12791765
KEYWORDS    EST.
SOURCE      human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 966)
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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JOURNAL  
COMMENT

Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr,  
Location/Qualifiers

FEATURES  
source

1..966  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DC023YO13"  
/clone\_lib="LTI\_NFL003\_NBC3"  
/sex="male"  
/tissue\_type="neuroblastoma cells"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT      243 a    247 c    285 g    179 t    12 others  
ORIGIN

Query Match                  10.4%;    Score 37.8;    DB 9;    Length 966;  
Best Local Similarity       53.1%;    Pred. NO. 2.2;  
Matches    78;    Conservative    1;    Mismatches    68;    Indels    0;    Gaps    0;

QY    172 GTGGACGCGTGAGGTGCTTTTCGCCATGACCCTCCTGGTTGTTGCAGTCACATTGCGCACG 231  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db    662 GGGATCGAGAGAGGTGGAGGTGAGTGACTGGCCATGGCTGTSTTCTGGACTTGTGGCAG 721  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY    232 CTTGCACCGTGACTCACTGCCCACATTGCCCGCGCGTGGCGGCCCTACAAAGCCAC 291  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db    722 CYGGACAGGGTCTGCTCTGGTTATTATACACGGAGCAGCTGCAGCTGCAACTGCCTC 781  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY    292 ACACGCACGCCGCGCACGATAACCCAT 318  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db    782 ATAGGACCGGCGCAGCAGCGACGCCCTT 808  
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6  
AZ551127/c  
LOCUS  
DEFINITION  
ENTDN1LTR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.  
ACCESSION  
AZ551127  
VERSION  
AZ551127.1 GI:11176428  
KEYWORDS  
GSS.  
SOURCE  
Entamoeba histolytica.  
ORGANISM  
Entamoeba histolytica  
Eukaryota; Entamoebidae; Entamoeba.  
REFERENCE  
1 (bases 1 to 969)  
Loftus,B., Van Aken,S. and Fraser,C.  
AUTHORS  
Determination of clone end sequences from Entamoeba histolytica  
TITLE  
HM1:IMSS sheared DNA library  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: bjloftus@tigr.org  
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library  
Seq primer: M13-Reverse  
Class: shotgun  
High quality sequence start: 325  
High quality sequence stop: 569.

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FEATURES
Source
Location/Qualifiers
1..969
/organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Borell, Oxford University Press, 1999)."
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BASE COUNT 251 a 152 c 250 g 316 t

ORIGIN

Query Match 10.2%; Score 37.4; DB 17; Length 969;

Best Local Similarity 57.1%; Pred. No. 2.9;

Matches 68; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 230 CGCTGACCGTGACTGACCTGCCACATGCCCCCGCGCGCGCTACAAAAGCC 289

Db 899 CTCGGGCACTGGCGATCCCCCGCCACGGCGCCCGCCCTCCCGCAGCGCC 840

QY 290 ACACAGCGACGCGCGCCAGGATACCCATCTCCATCCCGGTCCAGCAAGATCC 348

Db 839 AGCAACCCACCCAGTAGTATTCCTATCTCCATCCACCCAGCCAGCCCTCC 781

RESULT 7

AL553672

LOCUS

DEFINITION

AL553672 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CSODI078YF07 3

prime, mRNA sequence.

ACCESSION

AL553672

VERSION

AL553672.1 GI:12893722

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Li.W.B., Gruber.C., Jessee.J. and Polayes.D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Location/Qualifiers

1..777

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CSODI078YF07"

/clone\_lib="LTI\_NFL006\_PL2"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 200 a 199 c 240 g 135 t 3 others





```
/clone="L1922k"
/clone_lib="Leishmania major Friedlin Cosmid Genomic
Library"
/lab_host="E. coli ED8767"
/note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from
Leishmania major Friedlin was partially digested with
Sau3AI, size selected, and ligated with BamHI-digested
cLHYG cosmid vector DNA. 9216 clones were picked and
arrayed. Library construction is described in Ivens et
al., Genomics Research, 8:135-145 (1998). The cLHYG
vector (Acc. No. CVU59231) is described in Ryan et al,
Gene, 131:145-150 (1993)"
BASE COUNT      79 a      148 c      161 g      88 t
ORIGIN

Query Match      10.0%; Score 36.6; DB 17; Length 476;
Best Local Similarity 55.0%; Pred. No. 3.4;
Matches 72; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 146 CGTGCTACTGCTACATCCTGTAGACGGTGGACGGTGAGGTGCTTTCGCCATGACCGTCC 205
|| ||| ||||| ||| ||||| | ||| ||||| ||||| ||||| |||||
Db 339 CGCGCTGCTGCTTCAGCGGTGTAGATGTGCACGGCATCAAGTCCCGCCGCCACCGCTCG 280

QY 206 TTGGTTGTTGCAGTCACTTTGCGCAGCGTTTGACCGTGACTCACCTGCCACATTGCCCCCG 265
|| ||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||
Db 279 ATGAAGAGCGCGCTGCCCTCTTAGAGCTGCCGCTGGCTCTGCTGCAGGAGTGCCAGCG 220

QY 266 CCGTCGCCGC 276
|| || | ||
Db 219 CGTGCCATGC 209

RESULT 12
L2025Y/c
LOCUS
DEFINITION
Leishmania major Friedlin cosmid L2025 t7 end-sequence, genomic
survey sequence.
ACCESSION
AL354102
VERSION
AL354102.1 GI:7671716
KEYWORDS
GSS.
SOURCE
Leishmania major.
ORGANISM
Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
REFERENCE
1 (bases 1 to 493)
AUTHORS
Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and
Smith,D.F.
TITLE
A physical map of the Leishmania major Friedlin genome
JOURNAL
Genome Res. 8 (2), 135-145 (1998)
MEDLINE
98146435
PUBMED
9477341
REFERENCE
2 (bases 1 to 493)
AUTHORS
Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and
Barrell,B.G.
TITLE
Direct Submission
JOURNAL
Submitted (28-APR-2000) Leishmania major Friedlin genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
alicat@sanger.ac.uk
COMMENT
see http://www.ebi.ac.uk/parasites/leish.html
Details of Leishmania sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/L_major/
The cLHYG t7 primer sequence can be obtained from acc. no. U59231.
FEATURES
Location/Qualifiers
source
1..493
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="cosmid L2025"
BASE COUNT      84 a      154 c      168 g      87 t
ORIGIN

Query Match      10.0%; Score 36.6; DB 17; Length 493;
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/clone="L1922k"
/clone_lib="Leishmania major Friedlin Cosmid Genomic
Library"
/lab_host="E. coli ED8767"
/note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from
Leishmania major Friedlin was partially digested with
Sau3AI, size selected, and ligated with BamHI-digested
cLHYG cosmid vector DNA. 9216 clones were picked and
arrayed. Library construction is described in Ivens et
al., Genomics Research, 8:135-145 (1998). The cLHYG
vector (Acc. No. CVU59231) is described in Ryan et al,
Gene, 131:145-150 (1993)"
BASE COUNT      79 a      148 c      161 g      88 t
ORIGIN

Query Match      10.0%; Score 36.6; DB 17; Length 476;
Best Local Similarity 55.0%; Pred. No. 3.4;
Matches 72; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 146 CGTGCTACTGCTACATCCTGTAGACGGTGGACGGTGAGGTGCTTTCGCCATGACCGTCC 205
|| ||| ||||| ||| ||||| | ||| ||||| ||||| ||||| |||||
Db 336 CGCGCTGCTGCTTCAGCGGTGTAGATGTGCACGGCATCAAGTCCCGCCGCCACCGCTCG 277

QY 206 TTGGTTGTTGCAGTCACTTTGCGCAGCGTTTGACCGTGACTCACCTGCCACATTGCCCCCG 265
|| ||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||
Db 276 ATGAAGAGCGCGCTGCCCTCTTAGAGCTGCCGCTGGCTCTGCTGCAGGAGTGCCAGCG 217

QY 266 CCGTCGCCGC 276
|| || | ||
Db 216 CGTGCCATGC 206

RESULT 13
AL564785
LOCUS
DEFINITION
AL564785 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSODM007YD05 3
prime, mRNA sequence.
ACCESSION
AL564785
VERSION
AL564785.1 GI:12915538
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 916)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
source
1..916
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODM007YD05"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      227 a      232 c      276 g      173 t      8 others
ORIGIN

Query Match      10.0%; Score 36.6; DB 9; Length 916;
Best Local Similarity 53.1%; Pred. No. 5;
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 172 GTGGACGGTGAGGTGCTTTCGCCATGACCGTCCCTGGTTGTTCAGTCACTTGGCGCAG 231
|| ||| ||||| ||| ||||| | ||||| ||||| ||||| ||||| |
Db 595 GGGATCGAGAGAGGTGGAGTGAGGTGACTGGCCATGGCTGTATTCTGGACTTGTGGCAG 654

QY 232 CTTGCACCGTGACTCACCTGCCACATTGCCCGCGCGCTGCCGCGCCCTACAAAAGCCAC 291
|| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db 655 CTGGACACAGGTCTGCTCTGCGTAATTATACACGGAGCCAGCTGCAGCTGCAACTGCCTC 714

QY 292 ACACGCACGCCGCCACGATAACCCAT 318
|| || | ||
Db 715 ATAGGACCGGGCAGCAGCAGCGCGCTT 741
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